included age, HBe positivity, platelets, and levels of HBsAg, HBcrAg, HBV DNA and IL-22 before treatment. Statistical analyses were carried out using SPSS software version 21.0J (IBM Japan, Tokyo, Japan).

RESULTS

Baseline clinical characteristics of patients

THE CLINICAL PROFILE of the experimental patient cohort is shown in Table 1. Among our 48 patients with chronic hepatitis, 39 (81%) achieved a VR at 24 months. A VR was attained in 11 of 20 HBeAg positive patients (55%) and in all 28 HBeAg negative patients (100%). One patient (5%) demonstrated HBeAg seroclearance through to month 24, but did not attain HBeAg seroconversion. No patient experienced a virological breakthrough.

The median age of patients achieving a VR was significantly higher than that of patients who did not (55 vs 37 years; $P = 0.031$) (Table 1). In contrast, viral responders had significantly lower median HBsAg (3.3 vs 3.9 log IU/mL; $P = 0.001$) and HBcrAg (5.0 vs 6.8 log U/mL; $P < 0.001$) levels than non-responders. We found no significant differences between patient groups with regard to sex, HBV genotype, or albumin, AST, ALT, bilirubin or platelet levels. When stratified by HBeAg positivity, HBsAg level only was significantly associated with a VR (3.2 vs 3.9 log IU/mL; $P = 0.003$). When we compared HBeAg positive and negative patients, median HBV DNA and HBcrAg levels, but not HBsAg, were significantly higher in HBeAg positive patients (Table S1).

Detection and quantification of serum markers in patients with chronic hepatitis B and controls

Serum samples obtained prior to ETV therapy were examined for the presence of six cytokines and five chemokines by multiplex assays. As shown in Table 2, the median baseline serum concentrations of IL-6 (6.5 vs 5.8 pg/mL; $P = 0.031$) and three chemokines (CCL2 [39.3 vs 31.5 pg/mL; $P = 0.022$], CXCL9 [329.2 vs 127.8 pg/mL; $P = 0.002$] and CXCL10 [217.1 vs 58.7 pg/mL; $P = 0.001$]) were significantly higher in patients with chronic hepatitis B than in healthy controls. When we subdivided patients into HBeAg positive or anti-HBe positive groups, no significant differences in the median concentrations of any cytokine or chemokine were seen, including IL-22 (Table S1).

Effect of ETV therapy on serum cytokine levels

The median levels of serum cytokines and chemokines in our cohort are shown in Table 3. Among our patients, the median baseline serum IL-22 concentration was significantly higher in virological responders than in non-responders (35.3 vs 27.8 pg/mL; $P = 0.031$) (Fig. 1a). No other cytokines or chemokines were associated with

Table 1 Demographic and clinical characteristics of 48 patients with chronic hepatitis B

Characteristics	Total, $n = 48$	VR (+), $n = 39$	VR (−), $n = 9$	P
Age, years	55 (24–81)	55 (24–81)	37 (26–67)	**0.031**
Male, *n* (%)	33 (69)	29 (74)	4 (44)	0.18
HBeAg positive, *n* (%)	20 (42)	11 (28)	9 (100)	**<0.001**
HBV genotype C, *n* (%)	45 (94)	37 (95)	8 (89)	1.00
HBV DNA (log copies/mL)	6.6 (2.7 to >9.1)	6.4 (2.7 to >9.1)	8.0 (3.9 to >9.1)	0.06
HBsAg (log IU/mL)	3.4 (−1.2 to 4.5)	3.3 (−1.2 to 4.3)	3.9 (3.3–4.5)	**0.001**
HBcrAg (log U/mL)	5.2 (3.0–6.8)	5.0 (3.0–6.8)	6.8 (5.4–6.8)	**<0.001**
Albumin (mg/dL)	4.2 (2.3–5.3)	4.2 (3.1–5.3)	4.2 (2.3–4.5)	0.80
AST (IU/L)	48 (15–1476)	51 (15–1476)	36 (28–358)	0.82
ALT (IU/L)	49 (9–2021)	63 (9–2021)	56 (29–954)	0.74
Bilirubin (mg/dL)	0.8 (0.3–3.1)	0.8 (0.3–3.1)	0.7 (0.5–1.0)	0.33
Platelet (/μL)	16.3 (8.0–28.9)	15.2 (8.0–28.9)	19.5 (11.9–27.7)	0.053

Continuous variables are expressed as median values (range).
Bolded figures indicate statistical significance.
ALT, alanine aminotransferase; AST, aspartate aminotransferase; HBcrAg, hepatitis B core-related antigen; HBeAg, hepatitis B e-antigen; HBsAg, hepatitis B surface antigen; HBV, hepatitis B virus.

Table 2 Serum cytokines and chemokines in patients with chronic hepatitis B and healthy subjects

Cytokine/chemokine	Patients	Controls	*P*-value
IL-2	2.3 (0–4.9)	2.1 (1.9–2.4)	0.42
IL-6	6.5 (2.7–19.1)	5.8 (5.8–6.5)	**0.031**
IL-10	1.1 (0.0–26.8)	1.4 (1.3–1.6)	0.49
IL-12p70	12.9 (0.1–22.0)	12.9 (12.8–12.9)	0.50
IL-21	12.5 (5.0–1916.5)	11.5 (10.5–253.5)	0.68
IL-22	34.9 (27.2–75.7)	33.6 (32.3–39.0)	0.47
CCL2	39.3 (23.8–8118.8)	31.5 (26.7–39.3)	**0.022**
CCL3	4.8 (0.0–651.8)	7.0 (5.0–9.9)	0.25
CXCL9	329.2 (89.8–18 758.9)	127.8 (107.5–874.3)	**0.002**
CXCL10	217.1 (18.6–3594.3)	58.7 (24.7–859.5)	**0.001**
CXCL11	40.8 (0.7–553.8)	25.8 (12.9–90.3)	0.23

Continuous variables are expressed as median values (range) (pg/mL).
Bolded figures indicate statistical significance.
IL, interleukin.

a VR. When stratified by HBeAg positivity, serum IL-22 and IL-6 levels in the VR group were significantly higher than those in the non-VR group (35.3 vs 31.2 pg/mL [$P = 0.046$] and 6.9 vs 6.1 pg/mL [$P = 0.031$], respectively).

Several clinical findings (HBV DNA, HBsAg, HBcrAg, albumin, AST, ALT, bilirubin and platelet) at baseline were examined for their correlation with serum cytokines or chemokines in patients with chronic hepatitis B. Serum IL-6, CXCL9, CXCL10 and CXCL11 were all positively correlated with values for AST, ALT and bilirubin, but were negatively correlated with serum HBsAg (Table 4). CXCL9, CXCL10 and CXCL11 were also significantly correlated with each other (data not shown). There was a negative correlation between HBsAg and AST, ALT and bilirubin (data not shown).

Prediction of VR in patients with chronic hepatitis B

We performed ROC analysis to determine the optimal cut-off values for serum IL-22, HBsAg and HBcrAg in predicting a VR for chronic HBV infection with the values obtained from the 39 patients who achieved a VR and the nine who did not. The selection of optimal cut-off point values was based on the IL-22, HBsAg and HBcrAg levels at which accuracy was maximal. Optimal cut-off value, sensitivity, specificity, positive predictive value, negative predictive value and calculated area

Table 3 Serum cytokines and chemokines in treatment outcome to antiviral therapy

Cytokine/chemokine	VR	Non-VR	*P*-value
IL-2	2.3 (0.0–4.9)	3.1 (0.0–3.3)	0.60
IL-6	6.8 (2.7–19.1)	6.1 (4.3–12.5)	0.22
IL-10	0.6 (0.0–26.8)	1.5 (0.0–5.0)	0.86
IL-12p70	12.9 (0.1–22.0)	12.9 (1.2–18.0)	0.74
IL-21	12.2 (5.0–1916.5)	19.9 (5.9–27.8)	0.70
IL-22	35.3 (27.2–75.7)	27.8 (27.3–46.7)	**0.031**
CCL2	40.8 (24.4–118.8)	34.8 (23.8–60.3)	0.13
CCL3	4.5 (0.0–651.8)	6.5 (2.7–22.9)	0.57
CXCL9	322.5 (115.4–18 758.9)	353.6 (89.8–1545.1)	0.60
CXCL10	206.3 (29.1–3594.3)	294.2 (18.6–2240.7)	0.94
CXCL11	39.9 (0.7–553.8)	48.8 (12.6–428.2)	0.80

Continuous variables are expressed as median values (range) (pg/mL).
Bolded figure indicates statistical significance.
IL, interleukin; VR, virological response.

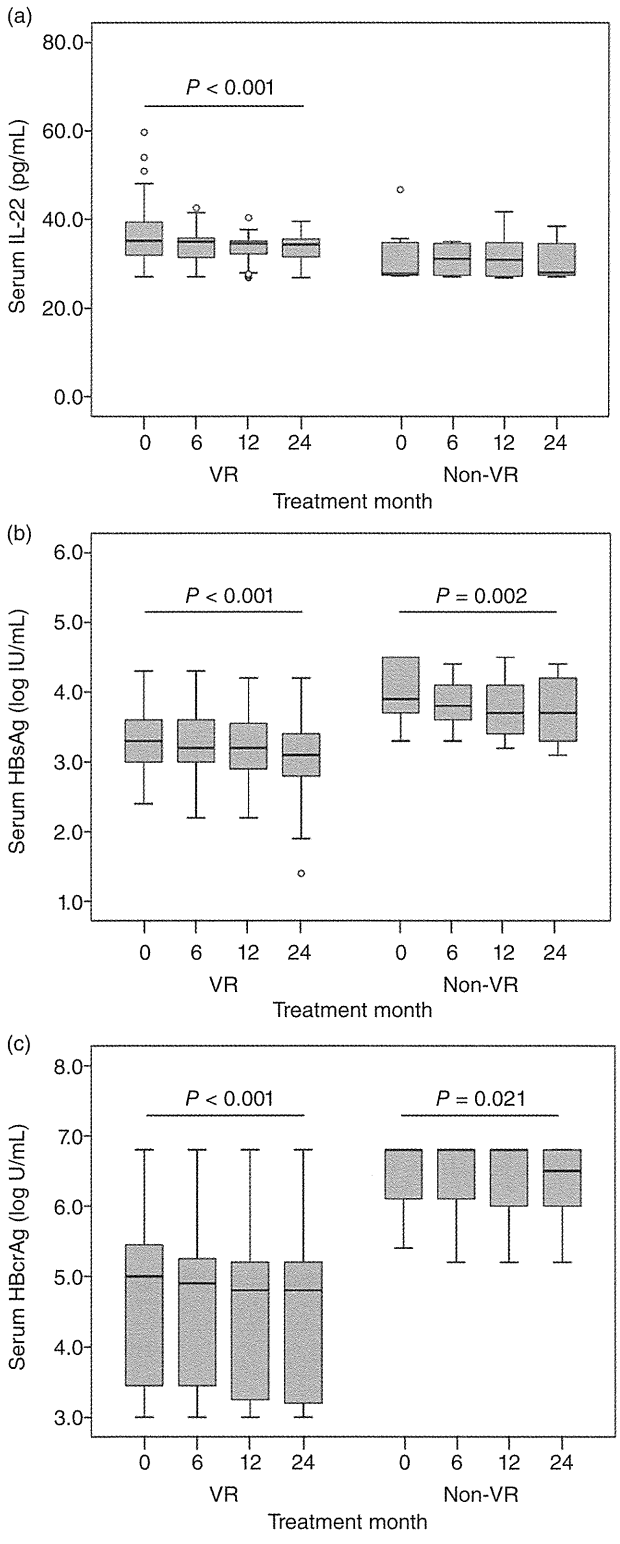

Figure 1 Comparison of serum (a) IL-22, (b) HBsAg and (c) HBcrAg levels during entecavir therapy in the VR ($n = 39$) and non-VR ($n = 9$) groups. Boxes represent the interquartile range of the data. The lines across the boxes indicate the median values. The harsh marks above and below the boxes indicate the 90th and 10th percentiles for each group, respectively. IL, interleukin; HBsAg, hepatitis B surface antigen; HBcrAg, hepatitis core-related antigen; VR, virological response.

under the curve (AUC) values for each parameter are listed in Table 5. The AUC values were consistently high and ranged between 0.731 (IL-22) and 0.858 (HBcrAg).

Several factors found in association with a VR to ETV therapy were evaluated for their independence by multivariate analysis. We determined that IL-22 of 27.8 pg/mL or more (hazard ratio [HR] = 13.67 [95% confidence interval [CI] = 1.05–178.11], $P = 0.046$) and HBcrAg of 5.7 log U/mL or less (HR = 10.88 [95% CI = 1.02–115.44], $P = 0.048$) were independent factors related to a VR. HBsAg did not have a significant independent association in this study ($P = 0.071$).

Serum cytokine and chemokine changes during treatment

Longitudinal analysis of IL-22, HBsAg and HBcrAg levels was carried out at 6, 12 and 24 months after the initiation of therapy and showed significant gradual reductions in IL-22 ($P < 0.001$, Friedman test), HBsAg ($P < 0.001$) and HBcrAg ($P < 0.001$) in samples collected from patients who achieved a VR (Fig. 1). We noted a higher median serum IL-22 concentration at month 6 in the VR group than in the non-VR group ($P = 0.012$), and there were significant differences at each time point for HBsAg (6 months, $P = 0.002$; 12 months, $P = 0.006$; and 24 months, $P = 0.004$) and HBcrAg (6 months, $P < 0.001$; 12 months, $P < 0.001$; and 24 months, $P < 0.001$) between responders and non-responders.

DISCUSSION

IN THE PRESENT study, we measured the levels of six cytokines and five chemokines in patients with chronic hepatitis B and analyzed their association with ETV therapy outcome using a bead-array multiplex immunoassay system. Four of our observations are noteworthy and require further comment. First, serum IL-6, CCL2, CXCL9 and CXCL10 concentrations were

Table 4 Correlation between cytokines, chemokines and clinical parameters

		IL-2	IL-6	IL-10	IL-12	IL-21	IL-22	CCL2	CCL3	CXCL9	CXCL10	CXCL11
HBV DNA	*r*	0.08	0.01	0.10	0.06	0.08	0.17	−0.13	0.01	−0.13	−0.10	0.20
	P	0.61	0.97	0.51	0.69	0.61	0.25	0.39	0.95	0.39	0.50	0.18
HBsAg	*r*	−0.99	−0.35	−0.14	0.22	−0.08	−0.05	−2.5	0.02	−0.78	−0.61	−0.32
	P	0.51	**0.015**	0.35	0.14	0.61	0.74	0.09	0.89	**<0.001**	**<0.001**	**0.025**
HBcrAg	*r*	0.04	0.05	−0.16	0.24	0.18	0.14	−0.13	0.14	−0.14	−0.15	0.11
	P	0.79	0.76	0.29	0.11	0.21	0.35	0.40	0.33	0.36	0.31	0.45
Albumin	*r*	0.17	0.02	0.17	−0.02	0.05	−0.02	0.12	0.08	0.13	−0.09	0.02
	P	0.25	0.91	0.24	0.89	0.75	0.88	0.40	0.60	0.39	0.53	0.91
AST	*r*	0.05	0.40	0.11	−0.11	−0.03	0.14	0.13	−0.07	0.78	0.75	0.36
	P	0.72	**0.004**	0.45	0.47	0.83	0.33	0.39	0.66	**<0.001**	**<0.001**	**0.013**
ALT	*r*	0.02	0.42	0.12	−0.11	−0.06	0.16	0.10	−0.08	0.69	0.71	0.46
	P	0.91	**0.003**	0.40	0.44	0.70	0.28	0.52	0.57	**<0.001**	**<0.001**	**0.001**
Bilirubin	*r*	−0.03	0.36	0.07	0.08	−0.03	0.13	0.27	−0.12	0.33	0.65	0.35
	P	0.83	**0.012**	0.64	0.58	0.84	0.38	0.07	0.42	**0.023**	**<0.001**	**0.015**
Platelet	*r*	0.08	0.12	0.15	−0.09	0.13	0.25	−0.05	0.19	0.31	0.04	0.13
	P	0.57	0.42	0.33	0.55	0.38	0.09	0.74	0.20	**0.033**	0.82	0.39

Bolded figures indicate statistical significance.
ALT, alanine aminotransferase; AST, aspartate aminotransferase; HBcrAg, hepatitis B core-related antigen; HBsAg, hepatitis B surface antigen; HBV, hepatitis B virus; IL, interleukin; *r*, Spearman's rank correlation.

higher in patients with chronic hepatitis B than in healthy subjects. Second, serum IL-22 concentration before treatment was significantly higher in patients achieving a VR to ETV therapy. In contrast, responders had lower serum levels of HBsAg and HBcrAg at baseline. Third, IL-22, HBsAg and HBcrAg decreased during treatment and remained low in patients with a VR. Fourth, serum IL-6, CXCL9, CXCL10 and CXCL11 were positively correlated with serum values of AST, ALT and bilirubin, but were negatively correlated with HBsAg.

Interleukin-6 is a well-recognized multifunctional cytokine that may reflect more active hepatic necroinflammation and be associated with chronic HBV infection severity. As in previous studies,[18,21] serum IL-6 was significantly higher in the HBV-infected group than in healthy controls and was positively correlated with such clinical parameters as transaminases and bilirubin. Hence, our data support that IL-6 is strongly associated with the severity of liver diseases.

CXCL9, CXCL10 and CXCL11 appear to be particularly important in chronic HCV infection by promoting the development of intrahepatic inflammation that leads to fibrogenesis.[22,23] These chemokines are also significantly elevated in patients with necroinflammatory activity of acute and chronic hepatitis C.[24,25] In our study, serum CXCL9 and CXCL10 were higher in patients with chronic HBV infection than in healthy individuals, which was in agreement with a previous

Table 5 Optimal cut-off value, sensitivity, specificity, AUC, and predictive value of serum IL-22, HBsAg and HBcrAg at baseline of treatment in 48 patients with chronic hepatitis B

	Cut-off value	Sensitivity (%) (95% CI)	Specificity (%) (95% CI)	AUC (95% CI)	PPV (%)	NPV (%)
IL-22	27.8 pg/mL	56 (21–86)	90 (76–97)	0.731 (0.533–0.929)	90	56
HBsAg	3.6 log IU/mL	78 (40–97)	77 (61–89)	0.838 (0.704–0.971)	44	94
HBcrAg	5.7 log U/mL	89 (52–100)	82 (67–93)	0.858 (0.754–0.962)	53	97

All AUC values were significantly higher than a 0.50 non-predictive value ($P < 0.01$ for all comparisons). Cut-off values were determined by constructing receiver–operator curves.
AUC, area under the curve; CI, confidence interval; HBcrAg, hepatitis core-related antigen; HBsAg, hepatitis B surface antigen; IL, interleukin; NPV, negative predictive value; PPV, positive predictive value.

report.[12] Moreover, the serum CXCR3-associated chemokines CXCL9, CXCL10 and CXCL11 were all well correlated with serum values of AST, ALT and bilirubin. Because we observed a significant correlation between these chemokines and IL-6, our findings suggest that CXCR3-associated chemokines may too contribute to necroinflammatory activity in chronic HBV infection. However, there were insufficient histological data in our study to assess whether IL-6 and CXCR3-associated chemokines were correlated with degree of fibrosis, in addition to a lack of biochemical evidence of inflammation. We furthermore showed a striking negative association between HBsAg concentration and levels of IL-6 and CXCR3-associated chemokines. As HBsAg was also negatively correlated with transaminases and bilirubin, this HBsAg decline may be linked to increased immunological activity.

Interestingly, this study demonstrated a beneficial role of IL-22 in achieving a VR during ETV therapy. IL-22 is an IL-10 family cytokine that is important for the modulation of tissue responses during inflammation and is expressed by many types of lymphocytes of both the innate and adaptive immune systems, most notably T-helper 17 cells, γδ T cells, natural killer cells and lymphoid tissue inducer-like cells. The IL-22 receptor is highly expressed on hepatocytes.[26,27] At present, several studies support a protective role of IL-22 in the prevention of hepatocellular damage, although there is evidence indicating dual protective and pathogenic roles for this cytokine in the liver.[17,28–30] Some groups have examined the association between IL-22 and liver fibrosis in humans and mice.[31,32] In one report, tumor-infiltrating lymphocytes in HCC exhibited elevated IL-22 expression, and these IL-22$^+$ lymphocytes promoted tumor growth and metastasis in mice.[33] Although human patients with chronic hepatitis B show increased percentages of T-helper 17 cells in the peripheral blood and liver and an increased concentration of IL-22 in the serum,[14,34] there have been no reports on treatment outcome in patients with chronic HBV infection during ETV therapy. In our study, IL-22 levels decreased over time in both the VR and non-VR groups, but they were consistently higher in the VR group. This difference in IL-22 levels between the two groups further supports the possibility that IL-22 may be important for the activation of immune cells that contribute to viral control. When stratified by HBe positivity, although IL-22 was still significantly associated with a VR, the number of patients was only 20 in this study. Further research is needed to clarify the association between IL-22 and treatment response.

Lastly, we uncovered that lower baseline serum HBsAg and HBcrAg levels were associated with a VR. HBcrAg assays measure serum levels of HB core, e and 22-kDa precore antigens simultaneously using monoclonal antibodies that recognize the common epitopes of these three denatured antigens.[35] Because this assay measures all antigens transcribed from the precore/core gene, it is regarded as core related.[36] The AUC values for baseline HBsAg and HBcrAg levels were high at 0.838 and 0.858, respectively. Several studies have shown that HBsAg is useful for the management of ETV therapy,[37,38] whereby an HBsAg decline is most profound in patients losing HBeAg detectability during treatment.[39] HBeAg positivity was also significantly associated with treatment outcome in the present study. However, because HBcrAg, but not HBsAg or HBeAg, was an independent factor related to a VR in multivariate analysis, our results indicated that serum HBcrAg quantitation may offer clinicians a new tool in predicting treatment outcome in HBV infection. Further investigation of large cohorts must be done to validate the significance of our findings.

With a VR at 12 months established as a parameter, 38 patients (79%) achieved this event. Serum IL-22, HBsAg and HBcrAg levels were all still significantly associated with a VR at 12 months. AUC values were as high as between 0.737 (IL-22) and 0.878 (HBcrAg). Furthermore, ALT normalization was achieved in 40 (83%) and 42 (88%) patients at 12 and 24 months, respectively. Although lower median pretreatment levels of HBsAg and HBcrAg were significantly associated with ALT normalization, there was no such statistically significant relation for IL-22 (data not shown).

In summary, a cytokine (IL-6) and several chemokines (CCL2, CXCL9 and CXCL10) were seen to be elevated in patients with chronic hepatitis B. Our results indicate that serum IL-6 and CXCR3-associated chemokines are correlated with liver injury, serum IL-22 is a useful biomarker for predicting a VR to ETV therapy, and a lower level of serum HBcrAg is related to a favorable response to antiviral therapy.

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SUPPORTING INFORMATION

ADDITIONAL SUPPORTING INFORMATION may be found in the online version of this article at the publisher's website:

Table S1 Demographic, clinical characteristics, and serum cytokines and chemokines in patients with hepatitis B e-antigen (HBeAg) positive and hepatitis B e-antigen (HBeAg) negative patients.

KIR, *HLA*, and *IL28B* Variant Predict Response to Antiviral Therapy in Genotype 1 Chronic Hepatitis C Patients in Japan

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Abstract

Natural killer cell responses play a crucial role in virus clearance by the innate immune system. Although the killer immunoglobulin-like receptor (KIR) in combination with its cognate human leukocyte antigen (HLA) ligand, especially *KIR2DL3-HLA-C1*, is associated with both treatment-induced and spontaneous clearance of hepatitis C virus (HCV) infection in Caucasians, these innate immunity genes have not been fully clarified in Japanese patients. We therefore investigated 16 KIR genotypes along with *HLA-B* and *-C* ligands and a genetic variant of interleukin (IL) 28B (rs8099917) in 115 chronic hepatitis C genotype 1 patients who underwent pegylated-interferon-α2b (PEG-IFN) and ribavirin therapy. *HLA-Bw4* was significantly associated with a sustained virological response (SVR) to treatment (P = 0.017; odds ratio [OR] = 2.50,), as was the centromeric A/A haplotype of *KIR* (P = 0.015; OR 3.37). In contrast, SVR rates were significantly decreased in patients with *KIR2DL2* or *KIR2DS2* (P = 0.015; OR = 0.30, and P = 0.025; OR = 0.32, respectively). Multivariate logistic regression analysis subsequently identified the *IL28B* TT genotype (P = 0.00009; OR = 6.87, 95% confidence interval [CI] = 2.62 - 18.01), *KIR2DL2/HLA-C1* (P = 0.014; OR = 0.24, 95% CI = 0.08 - 0.75), *KIR3DL1/HLA-Bw4* (P = 0.008, OR = 3.32, 95% CI = 1.37 - 8.05), and white blood cell count at baseline (P = 0.009; OR = 3.32, 95% CI = 1.35 - 8.16) as independent predictive factors of an SVR. We observed a significant association between the combination of *IL28B* TT genotype and *KIR3DL1-HLA-Bw4* in responders (P = 0.0019), whereas *IL28B* TT along with *KIR2DL2-HLA-C1* was related to a non-response (P = 0.0067). In conclusion, combinations of *KIR3DL1/HLA-Bw4*, *KIR2DL2/HLA-C1*, and a genetic variant of the *IL28B* gene are predictive of the response to PEG-IFN and ribavirin therapy in Japanese patients infected with genotype 1b HCV.

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Introduction

Hepatitis C virus (HCV) infection is a major cause of chronic liver disease worldwide. Chronic HCV infection often develops into chronic hepatitis, which may progress to liver cirrhosis and/or hepatocellular carcinoma (HCC)[1]. HCC is a leading cause of death from malignant neoplasms in Japan[2]. Since approximately 70% of Japanese HCC patients are infected with HCV, the successful eradication of this virus, defined as a sustained virological response (SVR), is considered important to decrease the incidence of HCC.

Natural killer (NK) cells are key components of the innate antiviral immune response that are controlled by a balance of activation and inhibitory receptors. NK cell activation receptors include C-type lectin-like receptors (NKG2C, NKG2D, and NKG2E), natural cytotoxicity receptors (NKp30, NKp44, and NKp46), and CD16, while known inhibitory receptors include killer cell immunoglobulin-like receptors (KIRs) and the CD94/NKG2 family, which also contains a C-type lectin-like receptor (NKG2A) [3,4]. Sixteen *KIR* genes and pseudogenes have been identified that are encoded by a family of genes located on human chromosome 19q13.4. One particular feature of *KIRs* is their substantial genetic diversity. Some inhibitory *KIRs*

recognize human leukocyte antigen (HLA) class I molecules as their ligands; *KIR2DL1* recognizes *HLA*-C group 2 (*HLA-C2*) allotypes having lysine at amino acid position 80, whereas *KIR2DL2* and KIR2DL3 recognize *HLA-C* group 1 (*HLA-C1*) allotypes having asparagine at amino acid position 80 [5]. *KIR2DL2* and *KIR2DL3* also recognize HLA-B*4601 acquiring the-C1 epitope by gene conversion [6]. Furthermore, *KIR3DL1* recognizes subsets of *HLA*-A and *HLA*-B allotypes having the -Bw4 epitope determined by amino acid positions 77-83 [7].

It has been well documented that certain KIR-HLA receptor-ligand combinations are associated with susceptibility to infectious diseases, such as HCV, as well as with disease progression and treatment response [8-15]. Recent reports have also identified a relationship between interleukin (IL) 28B gene polymorphisms and treatment and spontaneous resolution of HCV infection[16-19]. Dring et al. observed that the presence of *IL28B* gene polymorphisms and *KIR* genotypes synergized to increase the risk of chronic HCV infection[20], although this finding is under debate[21]. Suppiah et al. [22] recently reported that genotyping for *IL28B*, *HLA*-C, and *KIR* genes was useful for predicting HCV treatment response in patients of European descent. As these gene associations have not yet been studied in the Japanese population, we evaluated whether HLA-KIR interactions, in addition to an *IL28B* polymorphism, would influence the outcome of pegylated-interferon-α (PEG-IFN) and ribavirin therapy in Japanese patients with chronic hepatitis C.

Materials and Methods

Ethics statement

This study was approved by the ethical committee of Shinshu University School of Medicine, Matsumoto, Japan, and written informed consent was obtained from all participants. The study was conducted in accordance with the principles of the Declaration of Helsinki.

Subjects

One hundred and fifteen consecutive IFN-treatment-naïve patients with chronic hepatitis C were enrolled in this study. All subjects were seen at Shinshu University Hospital or one of its affiliated hospitals. The clinical and demographic characteristics of our cohort are shown in Table 1. Diagnosis of chronic hepatitis C was based on previously reported criteria [23]: 1) presence of serum HCV antibodies and detectable viral RNA; 2) absence of detectable hepatitis B surface antigen and antibody to the human immunodeficiency virus; and 3) exclusion of other causes of chronic liver disease or a history of decompensated cirrhosis or HCC. Serum levels of HCV RNA were determined using Cobas Amplicor assays (sensitivity: 50 IU/mL; Roche Diagnostic Systems, Tokyo, Japan). HCV genotypes were determined using INNO-LiPA HCV II kits (Innogenetics, Gent, Belgium). Alanine aminotransferase (ALT), aspartate aminotransferase (AST), and other relevant biochemical tests were performed using standard methods[24]. Liver fibrosis was assessed using the AST to platelet ratio index (APRI) in this study. APRI has been recognized as a noninvasive test to estimate the degree of liver fibrosis in chronic liver disease with HCV infection[25]. APRI was calculated for all study subjects as follows: AST/upper limit of normal (45 IU/L) × 100/platelet count (10^9/L). Patients received PEG-IFN-α2b (Pegintron; MSD KK, Tokyo, Japan; 1.5 μg/kg of body weight by subcutaneous injection once per week) and ribavirin (Rebetol; MSD KK; 600-1000 grams daily, according to body weight) for 48 weeks, as described previously[26]. Patients achieving a sustained HCV response were defined as those whose serum HCV RNA was undetectable 24 weeks after completing therapy. Patients who did not meet this criterion, who included non-responders and relapsers, were regarded as treatment failures.

Table 1. Clinical features of sustained and non-sustained virological response patients with chronic hepatitis C.

Characteristic	All	SVR	Non-SVR	*P*
	(n = 115)	(n = 56)	(n = 59)	
Age (yr)	60 (24 - 80)	59 (25 - 80)	60 (24 - 75)	0.43
Male	66 (57)	34 (61)	32 (54)	0.48
Alanine aminotransferase (IU/L)	46 (17 - 389)	48 (17 - 389)	45 (17 - 309)	0.81
Aspartate aminotransferase (IU/L)	43 (17 - 246)	42 (17 - 231)	43 (17 - 246)	0.49
White blood cells (/μL)	4410 (2280 - 8240)	4740 (2700 - 8170)	4070 (2280 - 8240)	0.011
Hemoglobin (g/dL)	14.4 (9.2 - 18.2)	15.1 (11.0 - 18.2)	13.9 (9.2 - 17.4)	0.002
Platelet count (10^4/μL)	15.9 (6.7 - 33.6)	16.6 (8.3 - 26.2)	15.6 (6.7 - 33.6)	0.30
APRI	0.89 (0.21 - 5.40)	0.59 (0.22 - 5.40)	0.66 (0.21 - 5.06)	0.41
HCV RNA ($\log_{10}$ IU/mL)	6.4 (5.0 - 7.3)	6.1 (5.0 - 6.8)	6.5 (5.0 - 7.3)	< 0.001

Data are expressed as median (range) or n (%) as appropriate. SVR, sustained virological response; HCV, hepatitis C virus

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HLA, KIR, and IL28B (rs8099917) Genotyping

Genomic DNA was isolated from whole blood samples using QuickGene-800 assays (Fujifilm, Tokyo, Japan). We genotyped *HLA*-B, *HLA*-C, and *KIR* using a Luminex multi-analyzer profiling system with a LAB type® HD and KIR SSO genotyping kit (One Lambda, Inc., Canoga Park, CA), which is based on PCR sequence-specific oligonucleotide probes[27]. Subjects were identified as having the B/x or A/A genotype as defined previously[28]. Genotypes for the centromeric (*Cen*) and telomeric (*Tel*) parts of the *KIR* locus were determined according to the presence or absence of one or more B haplotype-defining *KIR* genes. Thus, *Cen-A1* and *Tel-A1* were the centromeric and telomeric motifs, respectively, of the canonical *A KIR* haplotype in the present study, *Cen-B1* and *Cen-B2* were alternative centromeric motifs of common *B KIR* haplotypes, and *Tel-B1* was the common telomeric motif of *B* haplotypes[29]. For much of this analysis, *Cen-B1* and *-B2* were grouped together as *Cen-B*, whereas *Cen-A1* was shortened to *Cen-A* and *Tel-A1* to *Tel-A*, as reported

previously[30,31]. Genotyping of an *IL28B* SNP (rs8099917) was performed using a TaqMan 5' exonuclease assay with primers supplied by Applied Biosystems[32]. Probe fluorescence signals were detected using a TaqMan assay for Real-Time PCR (7500 Real Time PCR System, Applied Biosystems) according to the manufacturer's instructions.

Statistical Analysis

The Mann-Whitney *U* test was employed to analyze continuous variables. Pearson's chi-squared test was used for the analysis of categorical data. We adopted Fisher's exact test when the number of subjects was less than 5. The Bonferroni correction for multiple testing was applied to our data of KIR-HLA combinations using the number of comparisons performed by our primary factors of interest in Table 2 (i.e., 8 tests = 4 combinations × 2 comparisons between two groups). A P value of < 0.05 was considered to be statistically significant. Association strength was estimated by calculating the odds ratio (OR) and 95% confidence interval (CI). Our model was checked by regression diagnostic plots to verify normality, linearity of data, and constant variance. Stepwise logistic regression analysis with a forward approach was performed to identify independent factors associated with an SVR after continuous variables were separated into 2 categorical variables by each median value. Statistical analyses were performed using SPSS software version 21.0J (IBM, Tokyo, Japan). Sensitivity, specificity, positive predictive value (PPV), and negative predictive value (NPV) were calculated to determine the reliability of the predictors of therapy response.

Results

Patient Characteristics and Treatment Outcome

All patients in our test cohort were infected with HCV genotype 1b. Of the 115 patients receiving PEG-IFN-α2b and ribavirin therapy, 56 (49%) achieved an SVR. The remaining 59 patients were non-responders, 28 of whom experienced a relapse and 31 who were null responders. The median white blood cell count (P = 0.011) and hemoglobin value (P = 0.002) in the SVR group were significantly higher than those in the non-SVR group prior to treatment. HCV viral load at baseline was significantly associated with treatment outcome (P < 0.001).

Association of HLA and KIR with a Sustained Virological Response

We first determined the frequency of *HLA-Bw* and *HLA-C* alleles in SVR and non-SVR patients (Figure 1). The frequency of *HLA-Bw4Bw6* in responders was significantly higher than that in non-responders (55% [31/56] vs. 36% [21/59]; P = 0.033; OR = 2.24, 95% CI = 1.06 - 4.75). Conversely, patients with the *HLA-Bw6* homozygote had a higher non-SVR rate (32% [18/56] vs. 54% [32/59]; P = 0.017; OR = 0.40, 95% CI = 0.19 - 0.85). Overall, *HLA-Bw4* was associated with an SVR among patients (68% [38/56] vs. 46% [27/59]; P = 0.017; OR = 2.50, 95% CI = 1.17 - 5.35). The frequencies of HLA-C were not statistically significant. We further checked whether particular HLA-Bw or HLA-C alleles were beneficial to treatment outcome. The HLA-B*35:01 allele was more frequently found in patients with an SVR than in those without (13% [15/102] vs. 4% [5/118]; P = 0.014 [Pc = 0.36]; OR = 3.49, 95% CI = 1.23 - 9.97).

Table 2. Frequency of *IL28B* genotype, *KIR3DL1/HLA-Bw4*, and *KIR2DL2/HLA-C1* combinations in 56 patients with a sustained virological response (SVR) and 59 patients with a non-SVR to pegylated interferon and ribavirin therapy of chronic hepatitis C.

KIR3DL1/ HLA-Bw4	*KIR2DL2/HLA-C1*	SVR	Non-SVR	P (Pc)	OR (95% CI)
		(n = 56)	(n = 59)		
+/+	+/+	5 (9%)	7 (12%)	0.61	
+/+	Other	31 (55%)	19 (32%)	0.012 (0.1)	2.61 (1.22 - 5.58)
Other	+/+	1 (2%)	10 (17%)	0.014 (0.12)	0.09 (0.01 - 0.72)
Other	Other	19 (34%)	23 (39%)	0.57	
IL28B	*KIR3DL1/ HLA-Bw4*	SVR	Non-SVR	P (Pc)	OR (95% CI)
		(n = 56)	(n = 59)		
TT	+/+	27 (48%)	13 (22%)	0.003 (0.024)	3.29 (1.47 - 7.39)
TT	Other	17 (30%)	14 (24%)	0.42	
TG/GG	+/+	9 (16%)	13 (22%)	0.42	
TG/GG	Other	3 (5%)	19 (32%)	0.00062 (0.0005)	0.12 (0.03 - 0.43)
IL28B	*KIR2DL2/ HLA-C1*	SVR	Non-SVR	P (Pc)	OR (95% CI)
		(n = 56)	(n = 59)		
TT	Other	38 (68%)	18 (31%)	0.000062 (0.0005)	4.81 (2.19 - 10.58)
TT	+/+	6 (11%)	9 (15%)	0.47	
TG/GG	Other	12 (21%)	24 (41%)	0.026 (0.21)	0.40 (0.17 - 0.91)
TG/GG	+/+	0 (0%)	8 (14%)	0.013 (0.1)	-

Data are expressed as n (%).

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The distribution of *KIR* genes and their association with treatment outcome are shown in Figure 2. No statistically significant differences were found for any allele combination apart from *KIR2DL2* and *KIR2DS2*; patients with these genes had significantly decreased SVR frequencies compared with those without (P = 0.015 [Pc = 0.48]; OR = 0.30, 95% CI = 0.11 - 0.82 and P = 0.025 [Pc = 0.8]; OR = 0.32, 95% CI = 0.12 - 0.90, respectively).

KIR genotype profiles were determined by the presence or absence of each *KIR* locus in patients (Figure 3). Since strong linkage disequilibrium is a prominent feature in the *KIR* region, *KIR* gene profiles were classified based on *Cen* and *Tel* motifs. When we evaluated SVR according to genotype and *Cen* and *Tel* frequencies, we observed that virologic clearance with *Cen-A/A* was significantly higher than that without (54% [50/92] vs.

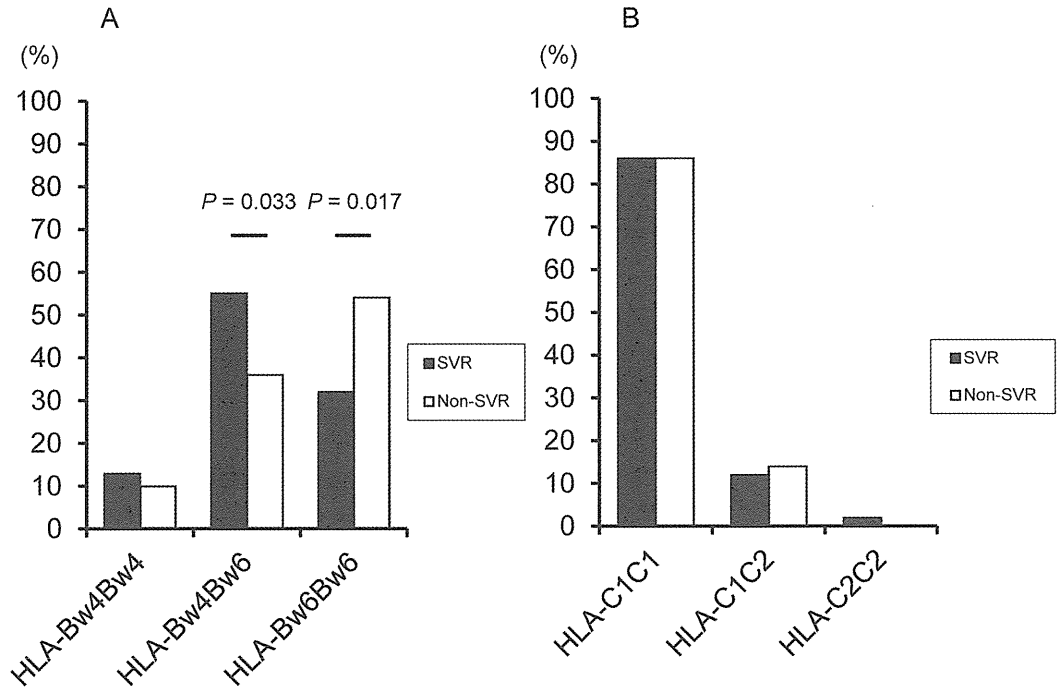

Figure 1. Frequency of *HLA-Bw* and -C alleles in 56 patients with a sustained virological response (SVR) and 59 patients with a non-SVR to pegylated interferon and ribavirin therapy of chronic hepatitis C.

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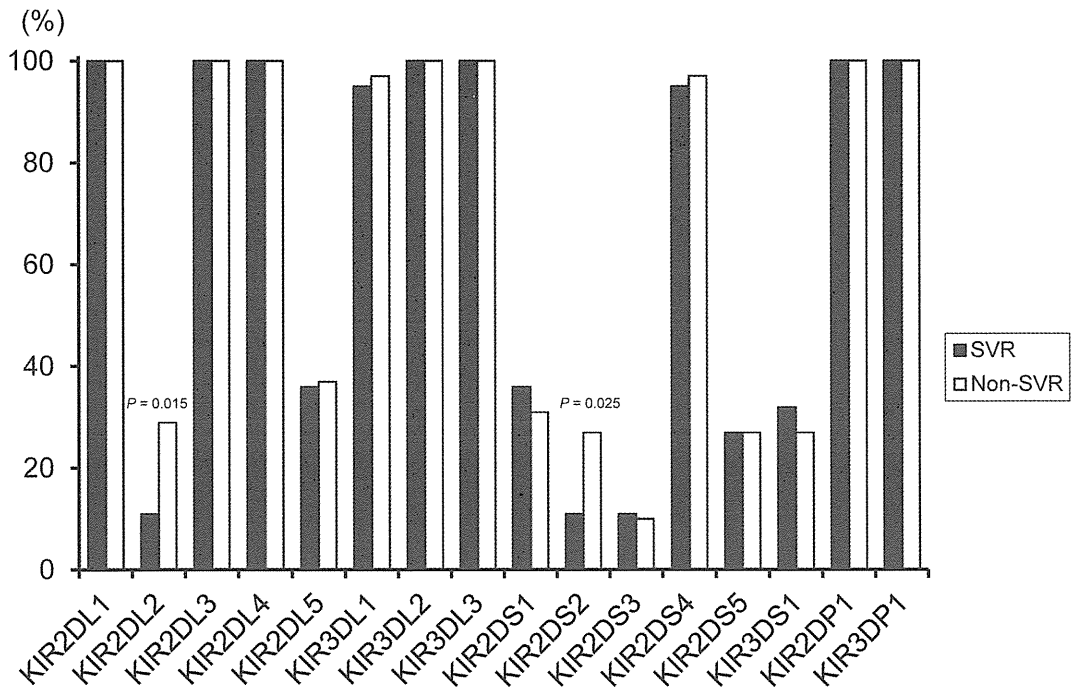

Figure 2. Frequency of each *KIR* gene in 56 patients with a sustained virological response (SVR) and 59 patients with a non-SVR to pegylated interferon and ribavirin therapy of chronic hepatitis C.

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26% [6/23], $P = 0.015$; OR = 3.37, 95% CI = 1.22 - 9.33). There were no significant differences regarding *AA* genotype and *Tel*.

We next analyzed combinations of activation/inhibitory *KIR*s and their *HLA* ligands for possible associations with an SVR. Among the combinations of *KIR3DL1-HLA-Bw4*, *KIR2DL2-HLA-C1*, and KIR2DL1-*HLA*-C2, patients who carried the inhibitory *KIR3DL1* receptor and its ligand *HLA-Bw4* had a significantly higher response rate than those without *KIR3DL1* or *HLA-Bw4* (58% [36/62] vs. 38% [20/53]; $P = 0.030$ [$Pc = 0.12$]; OR = 2.29, 95% CI = 1.08 - 4.84). In contrast, the *KIR2DL2-HLA-C1* combination resulted in a significantly lower SVR rate (26% [6/23] vs. 54% [50/92]; $P = 0.015$ [$Pc = 0.06$]; OR = 0.30, 95% CI = 0.11 - 0.82). Although several studies have found that *KIR2DL3-HLA-C1* carriers are associated with treatment-induced and spontaneous clearance of HCV in Caucasians, no such association was found in our cohort (data not shown).

Patients with *KIR3DL1-HLA-Bw4* but without *KIR2DL2-HLA-C1* had a higher SVR rate (55% [31/56] vs. 32% [19/59]; $P = 0.012$ [$Pc = 0.1$]; OR = 2.61, 95% CI = 1.22 - 5.58) (Table 2). Conversely, the frequency of the *KIR2DL2-HLA-C1* positive, but *KIR3DL1-HLA-Bw4* negative condition was significantly higher in non-responders (17% [10/59] vs. 2% [1/56]; P = 0.014 [$Pc = 0.12$]; OR = 0.09, 95% CI = 0.01 - 0.72).

Prediction of a Sustained Virological Response by KIR-HLA and IL28B

Examination of the *IL28B* rs8099917 SNP in our cohort revealed significant differences in SVR frequencies. The SVR rate in patients with the *IL28B* TT genotype was significantly higher in those with TG or GG genotypes (62% [44/71] vs. 27% [12/44), $P = 0.0003$; OR = 4.35, 95% CI = 1.92 - 9.85). In subjects with *IL28B* TT and *KIR3DL1-HLABw4*, virologic clearance was significantly increased over other combinations (68% [27/40] vs. 39% [29/75]; $P = 0.003$ [$Pc = 0.024$]; OR 3.29, 95% CI = 1.47 - 7.39).

We next evaluated several factors found in association with an SVR to PEG-IFN and ribavirin therapy for independence by logistic regression analysis. Fifty-six responders were compared with 59 non-responders by means of a forward stepwise likelihood ratio logistic regression method; estimated OR coefficients, 95% CI, and *P* values are summarized in Table 3 for the variables that remained in equation at the last step. *IL28B* TT genotype ($P = 0.00009$; OR = 6.87, 95% CI = 2.62 - 18.01), *KIR2DL2-HLA*-C1 ($P = 0.014$; OR = 0.24, 95% CI = 0.08 - 0.75), white blood cell count ≥ 4410/μL ($P = 0.009$; OR = 3.32, 95% CI= 1.35 - 8.16), and *KIR3DL1-HLA-Bw4* ($P = 0.008$; OR = 3.32, 95% CI = 1.37 - 8.05) were all identified as independent parameters that significantly influenced an SVR.

The frequency of the *IL28B* TT genotype with *KIR3DL1-HLA-Bw4* in responders was significantly higher than in non-responders (48% [27/56] vs. 22% [13/59]; $P = 0.003$ [$Pc = 0.024$]; OR = 3.29, 95% CI = 1.47 - 7.39) (Table 2). Patients with the *IL28B* TT genotype without *KIR2DL2-HLA-C1* had a significantly higher SVR rate (68% [38/56] vs. 31% [18/59]; $P = 0.000062$ [$Pc = 0.0005$]; OR = 4.81, 95% CI = 2.19 - 10.58). The frequency of a non-SVR was significantly higher in patients with the *IL28B* non-TT genotype both with and without

KIR profile	Geno type	Cen motif	Tel motif	3DL3	2DS2	2DL2	2DL3	2DP1	2DL1	3DP1	2DL4	3DL1	3DS1	2DL5	2DS3	2DS5	2DS1	2DS4	3DL2	SVR (n = 56)	Non-SVR (n = 59)
1	AA	A/A	A/A	+	-	-	+	+	+	+	+	+	-	-	-	-	-	+	+	34 (60.7)	28 (47.5)
2	Bx	A/A	A/B	+	-	-	+	+	+	+	+	+	+	+	-	+	+	+	+	9 (16.1)	10 (16.9)
3	Bx	A/B	A/A	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+	+	2 (3.6)	8 (13.6)
4	Bx	A/A	A/B	+	-	-	+	+	+	+	+	+	+	+	+	-	+	+	+	4 (7.1)	2 (3.4)
5	Bx	A/A	B/B	+	-	-	+	+	+	+	+	-	+	+	-	+	+	-	+	3 (5.4)	1 (1.7)
6	Bx	A/B	A/B	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	1 (1.8)	2 (3.4)
7	Bx	A/B	A/B	+	+	+	+	+	+	+	+	+	-	+	-	+	+	+	+	1 (1.8)	2 (3.4)
8	Bx	A/B	A/A	+	+	+	+	+	+	+	+	+	-	+	+	-	-	+	+	0 (0.0)	3 (5.1)
9	Bx	A/B	A/B	+	+	+	+	+	+	+	+	+	-	+	+	-	+	+	+	1 (1.8)	0 (0.0)
10	Bx	A/B	A/B	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	1 (1.8)	0 (0.0)
11	Bx	A/B	B/B	+	+	+	+	+	+	+	+	-	+	+	-	+	+	-	+	1 (1.8)	0 (0.0)
12	Bx	A/B	A/A	+	-	+	+	+	+	+	+	+	-	-	-	-	-	+	+	0 (0.0)	1 (1.7)
13	Bx	A/A	A/A	+	-	-	+	+	+	+	+	+	-	+	+	-	-	+	+	0 (0.0)	1 (1.7)

Figure 3. *KIR* gene profile frequencies in 56 patients with a sustained virological response (SVR) and 59 patients with a non-SVR to pegylated interferon and ribavirin therapy of chronic hepatitis C. Numerical data represent the number of individuals (%). The presence of *KIR* genes is indicated by gray shading. Cen, centromeric; Tel, telomeric.

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Table 3. Logistic regression analysis of variables contributing to a sustained virological response to pegylated interferon and ribavirin.

Factor	Odds ratio	95% confidence interval	*P*
IL28B TT genotype	6.87	2.62 - 18.01	0.00009
KIR2DL2/HLA-C1	0.24	0.08 - 0.75	0.014
White blood cells ≥ 4410/μL	3.32	1.35 - 8.16	0.009
KIR3DL1/HLA-Bw4	3.32	1.37 - 8.05	0.008

Only variables achieving statistical significance ($P < 0.05$) in multivariate logistic regression analysis are shown.

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KIR2DL2-HLA-C1 (14% [8/59] vs. 0% [0/8]; $P = 0.013$ [$Pc = 0.1$] and 41% [24/59] vs. 21% [12/56]; $P = 0.026$ [$Pc = 0.21$]; OR = 0.40, 95% CI = 0.17 - 0.91, respectively). The ability to predict an SVR by *IL28B* genotype and *KIR3DL1-HLA-Bw4* and *KIR2DL2-HLA-C1* was next evaluated. Corresponding values for sensitivity, specificity, PPV, and NPV are listed in Table S1 in File S1. A combination of the *IL28B* TT genotype and *KIR3DL1-HLA-Bw4* demonstrated high predictive specificity (78%), as did the combination of *IL28B* TT genotype and *KIR2DL2-HLA-C1* (86%).

Lastly, we analyzed combinations of the three factors of *IL28B* genotype, *KIR3DL1-HLA-Bw4*, and *KIR2DL2-HLA-C1* for prediction of treatment outcome (Table S2 in File S1). The frequencies of *IL28B* TT, *KIR2DL2-HLA-C1*-negative, with and without *KIR3DL1-HLA-Bw4* were significantly higher among responders (38% [21/56] vs. 19% [11/59]; P = 0.024 [Pc = 0.29]; OR = 2.62, 95% CI = 1.12 - 6.12 and 30% [17/56] vs. 12% [7/59]; P = 0.015 [Pc = 0.18]; OR = 3.24, 95% CI = 1.22 - 8.57, respectively).

Discussion

The present study examined *HLA*, *KIR*, and *IL28B* gene variant associations with an SVR following PEG-IFN and ribavirin therapy in Japanese patients with chronic hepatitis C. We found a significant association of *HLA-Bw* alleles with treatment outcome, although the frequency of *HLA-C* alleles did not differ significantly between responders and non-responders. Functional analyses have demonstrated that NK cells in *HLA-C1C1* subjects exhibit a more rapid and stronger antiviral response that those in *HLA-C2C2* subjects due to differing responses of *HLA-C*-inhibited NK subsets[33]. *HLA-C2C2* homozygousity is strongly associated with treatment failure in HCV patients of European ancestry [11,22], but we could not assess its role in our study because this genotype was found in only 1 of 115 patients.

We uncovered a significant association between the presence of *KIR2DL2* or *KIR2DS2* and lower SVR rates. Several reports have shown that *KIR2DL3-HLAC1* in Caucasians [11,22] and *KIR2DL5* in Brazilians [34] are associated with treatment outcome of antiviral therapy. Since our results showed no such statistical significances, these conflicting interpretations may reflect differences in patient selection, genetic background, sample size, and/or treatment regimen. Further studies are required to clarify this discrepancy in the Japanese population.

A study by Dring et al. examined *KIR* haplotypes in patients with HCV infection and showed that a centromeric *KIR* haplotype was increased in chronic HCV infection as compared with resolved cases [20]. We therefore determined *KIR* haplotypes and *Cen-A/B* and *Tel-A/B* in our patients as well, and found an interesting association between *Cen-A/A* and an SVR to antiviral therapy (P = 0.015; OR 3.37). Since *Cen-A/B* is determined by *KIR2DL3* and *KIR2DS2* and/or *KIR2DL2*, this finding is consistent with our results demonstrating a relationship between *KIR2DS2* and *KIR2DL2* genotypes and treatment failure.

The most significant finding in this study was the association between KIR-HLA receptor-ligand pairings and treatment outcome in chronic hepatitis C. Among the inhibitory KIR-HLA receptor-ligand pairs, patients with *KIR3DL1-HLA-Bw4* exhibited a significantly higher SVR rate when compared to those without this pair (P = 0.03; OR 2.29). Conversely, virologic clearance in patients with *KIR2DL2-HLA-C1* was significantly lower than in those without (P = 0.015; OR = 0.30). Stratification analysis of the 4 groups of *KIR3DL1-HLA-Bw4* (presence or absence) and *KIR2DL2-HLA-C1* (presence or absence) revealed a higher frequency of responders with *KIR3DL1-HLA-Bw4* presence, *KIR2DL2-HLA-C1* absence compared with those possessing *KIR2DL2-HLA-C1* presence, *KIR3DL1-HLA-Bw4* absence (62% vs. 9%; P = 0.0044; OR =16.32). When these KIR-HLA pairs were both either positive or negative, SVR rates were similar at 42% and 45%, respectively. Together with the results of logistic regression analysis, we clearly showed that *KIR3DL1-HLA-Bw4* was positively associated with an SVR (OR = 3.32) and that *KIR2DL2-HLA-C1* had a negative association (OR = 0.24) with treatment outcome. As almost one half of the Japanese population have the functional *KIR3DL1-HLA-Bw4* combination, this inhibitory receptor-ligand interaction is potentially important in understanding NK cell diversification. The NK-cell surface expression of KIR3DL1 is higher in individuals having Bw4 than in those lacking it [35]. Therefore, these cells might be more weakly controlled by inhibitory signals than other NK cells, more easily activated by viral infection, and more readily promoted for cytolysis and IFN-gamma production.

This study confirmed that the *IL28B* TT genotype is a strong predictor of an SVR in Japanese patients[18,32]. Furthermore, SVR frequencies were positively correlated with a combination of the *IL28B* TT genotype and *KIR3DL1-HLA-Bw4* (P = 0.0019) and negatively associated with the *IL28B* TT genotype and *KIR2DL2-HLA-C1* (P = 0.0067). These combinations were also highly specific for virologic response prediction. In light of these findings, patients with poor expected treatment outcome may be advised to wait for the use of combinations of direct acting antiviral agents[36]. Akuta et al. reported that a combination of amino acid substitutions in the core region of HCV and *IL28B* genotype was a useful predictor of PEG-IFN, ribavirin, and telaprevir therapy results in Japan[37]. Since we could not collect sera before treatment for all patients, we were not able to assess the effect of amino acid substitutions in the HCV core region. Furthermore, interferon-free combinations of direct-acting antiviral agents have become an area of considerable clinical interest. Chu et al. have reported that IL28B genotype appears to affect early viral kinetics in patients with chronic hepatitis C receiving interferon-free treatment [38]. Recently, two groups have discovered *IFN* lambda *4* (*IFNL4*), a new gene that may account for associations of spontaneous and IFN-based treatment clearance of HCV [39,40]. The IFN-λ 4 protein is generated by individuals who carry the ΔG allele of the ss469415590 variant, and the presence of this protein is strongly associated with impaired clearance of HCV. Linkage disequilibrium is strong between the *IFNL4-ΔG* allele and the unfavorable rs12979860-T allele (*IL28B*) in subjects of European or Asian ancestry, whereas this linkage disequilibrium is moderate in individuals of African ancestry [39]. We have confirmed that the linkage disequilibrium between the *IFNL4-ΔG* allele and *IL28B* SNP (rs8099917) is high and that the *IFNL4-ΔG* allele is strongly associated with treatment failure of PEG-IFN and ribavirin therapy in patients with Japanese chronic hepatitis C [41]. Hence, the clinical impacts of HLA-KIR genetic variants, IL28B genotype, and the IFNL4 allele should be explored.

In conclusion, the present study showed significant associations of *KIR3DL1-HLA-Bw4*, *KIR2DL2-HLA-C1*, and *IL28B* combinations with an SVR to PEG-IFN and ribavirin therapy in Japanese patients with genotype 1 HCV. The clinical significance of *IL28B* genotyping combined with HLA/KIR pairs to predict treatment outcome warrants further validation for triple therapy.

Supporting Information

File S1. Table S1, Sensitivity, specificity, and predictive values of IL28B TT genotype and KIR3DL1/HLA-Bw4 or

KIR2DL2/HLA-C1 for a sustained virological response in 115 patients with chronic hepatitis C. Data are expressed as % (n). PPV, positive predictive value; NPV, negative predictive value. Table **S2**, Frequency of ***IL28B*** genotype and ***KIR3DL1/HLA-Bw4*** and ***KIR2DL2/HLA-C1*** combinations in 56 patients with a sustained virological response (SVR) and 59 patients with a non-SVR to pegylated interferon and ribavirin therapy of chronic hepatitis C. Data are expressed as n (%).
(DOC)

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Author Contributions

Conceived and designed the experiments: YN TU ET MO. Performed the experiments: YN TU YK MO. Analyzed the data: YN TU YK MO. Contributed reagents/materials/analysis tools: YN TU SJ YK SS TK SM MK AM ET. Wrote the manuscript: TU MO.

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The Bcl-2 Homology Domain 3 (BH3)-only Proteins Bim and Bid Are Functionally Active and Restrained by Anti-apoptotic Bcl-2 Family Proteins in Healthy Liver*[S]

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Background: A fine balance between the anti- and pro-apoptotic multidomain Bcl-2 family proteins controls hepatocyte apoptosis in the healthy liver.
Results: Disruption of the BH3-only proteins Bim and Bid prevents spontaneous hepatocyte apoptosis in the absence of anti-apoptotic Bcl-2 family proteins.
Conclusion: Hepatocyte integrity is maintained by the well orchestrated Bcl-2 network.
Significance: We demonstrated the novel involvement of BH3-only proteins in the healthy Bcl-2 network of the liver.

An intrinsic pathway of apoptosis is regulated by the B-cell lymphoma-2 (Bcl-2) family proteins. We previously reported that a fine rheostatic balance between the anti- and pro-apoptotic multidomain Bcl-2 family proteins controls hepatocyte apoptosis in the healthy liver. The Bcl-2 homology domain 3 (BH3)-only proteins set this rheostatic balance toward apoptosis upon activation in the diseased liver. However, their involvement in healthy Bcl-2 rheostasis remains unknown. In the present study, we focused on two BH3-only proteins, Bim and Bid, and we clarified the Bcl-2 network that governs hepatocyte life and death in the healthy liver. We generated hepatocyte-specific Bcl-xL- or Mcl-1-knock-out mice, with or without disrupting Bim and/or Bid, and we examined hepatocyte apoptosis under physiological conditions. We also examined the effect of both Bid and Bim disruption on the hepatocyte apoptosis caused by the inhibition of Bcl-xL and Mcl-1. Spontaneous hepatocyte apoptosis in Bcl-xL- or Mcl-1-knock-out mice was significantly ameliorated by Bim deletion. The disruption of both Bim and Bid completely prevented hepatocyte apoptosis in Bcl-xL-knock-out mice and weakened massive hepatocyte apoptosis via the additional *in vivo* knockdown of *mcl-1* in these mice. Finally, the hepatocyte apoptosis caused by ABT-737, which is a Bcl-xL/Bcl-2/Bcl-w inhibitor, was completely prevented in Bim/Bid double knock-out mice. The BH3-only proteins Bim and Bid are functionally active but are restrained by the anti-apoptotic Bcl-2 family proteins under physiological conditions. Hepatocyte integrity is maintained by the dynamic and well orchestrated Bcl-2 network in the healthy liver.

Apoptosis via the intrinsic pathway, which is known as the mitochondrial pathway, is regulated by Bcl-2 family members. These members are divided into two groups as follows: core Bcl-2 family proteins, which possess three or four Bcl-2 homology domains (BH1–BH4)[2] and the Bcl-2 homology domain 3 (BH3)-only proteins (1). The former, which are multidomain proteins, are subdivided into pro- and anti-apoptotic proteins. Pro-apoptotic core Bcl-2 family members, such as Bax and Bak, serve as effector molecules of this apoptotic machinery. Upon activation, these members can form pores to permeabilize the mitochondrial outer membrane. Apoptogenic factors, such as cytochrome *c*, can then be released through this membrane into the cytosol, leading to the activation of the caspase cascade and to cellular demise (2). Anti-apoptotic core Bcl-2 family members, including Bcl-2, Bcl-xL, Mcl-1, Bcl-w, and Bfl-1/A1, inhibit the intrinsic pathway of apoptosis by either directly or indirectly antagonizing Bak/Bax activity (3–5). In the original rheostasis model, cellular life and death are regulated by a balance between these anti- and pro-apoptotic core Bcl-2 family proteins (6). We previously reported that the hepatocyte-specific deletion of the *bcl-x* gene resulted in spontaneous hepatocyte apoptosis, and this effect could be completely prevented by the additional deletion of the *bak* and *bax* genes (7). These findings elucidated the importance of the rheostatic balance of the core Bcl-2 family proteins in controlling hepatocyte apoptosis in the healthy liver.

The BH3-only proteins, which include at least eight members, are considered to function as pro-apoptotic sensors, and these proteins set this rheostatic balance toward apoptosis upon activation by a variety of apoptotic stimuli (8, 9). It has been reported that hepatocyte apoptosis through the activation of these BH3-only proteins is involved in the pathophysiology of various liver diseases (10–12). Alternatively, we previously reported that the slight activation of Bid, which can trigger hepatocyte apoptosis, occurs even in the healthy liver and that the inactivation of Bid partially ameliorated spontaneous hepato-

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[2] The abbreviations used are: BH1–BH4, Bcl-2 homology domains 1–4; SCID, severe combined immune deficiency; ALT, alanine aminotransferase.

cyte apoptosis in Bcl-xL- or Mcl-1-knock-out mice (7, 13). In the present study, we focused on another BH3-only protein, Bim, which promotes hepatocyte apoptosis upon activation by free fatty acids or by reactive oxygen species in pathological settings, and we further clarified the orchestration of the Bcl-2 network, which governs hepatocyte life and death in the physiological state (10, 11, 14, 15). We found that the disruption of Bim ameliorated hepatocyte apoptosis in Bcl-xL- or Mcl-1-knock-out mice, indicating the involvement of Bim in this hepatocyte apoptosis machinery in the healthy liver as well as that of Bid. Additionally, the deletion of both Bim and Bid prevented the massive hepatocyte apoptosis caused by the inhibition of both Bcl-xL and Mcl-1, suggesting that Bim and Bid are functionally active in the healthy liver and are essential regulators for promoting the intrinsic pathway of apoptosis in hepatocytes in the absence of anti-apoptotic Bcl-2 family proteins. Our present study unveiled the fine and dynamic Bcl-2 networks, the orchestration of which determines hepatocyte life and death in the healthy liver.

EXPERIMENTAL PROCEDURES

Mice—Mice carrying a *bcl-x* gene with two *loxP* sequences at the promoter region and a second intron (*bcl-x*$^{flox/flox}$), mice carrying an *mcl-1* gene encoding amino acids 1–179 flanked by two *lox*P sequences, and heterozygous *alb-cre* transgenic mice expressing the Cre recombinase gene under regulation of the *albumin* gene promoter have been described previously (16–18). Hepatocyte-specific Bcl-xL-knock-out mice (*bcl-x*$^{flox/flox}$*alb-cre*) (17), hepatocyte-specific Mcl-1-knock-out mice (*bcl-x*$^{flox/flox}$*alb-cre*) (13), systemic Bid-knock-out mice (*bid*$^{-/-}$) (12), and Bcl-xL/Bid double knock-out mice (*bid*$^{-/-}$*bcl-x*$^{flox/flox}$*alb-cre*) (7) have also been described previously. We purchased C57BL/6J mice from Charles River (Osaka, Japan), systemic Bim-knock-out mice (*bim*$^{-/-}$) from the Jackson Laboratory (Bar Harbor, ME), and NOD/ShiJic-*scid* Jcl mice from Clea Japan Inc. (Osaka, Japan). We generated Bcl-xL/Bim double knock-out mice (*bim*$^{-/-}$*bcl-x*$^{flox/flox}$*alb-cre*), Mcl-1/Bim double knock-out mice (*bim*$^{-/-}$*mcl-1*$^{flox/flox}$*alb-cre*), Bcl-xL/Bim/Bid triple knock-out mice (*bim*$^{-/-}$*bid*$^{-/-}$*bcl-x*$^{flox/flox}$*alb-cre*), and Bim/Bid double knock-out mice (*bim*$^{-/-}$*bid*$^{-/-}$) by mating the strains. We generated mice with a hepatocyte-specific deletion of Mcl-1 and homozygote severe combined immune deficiency (SCID) mutations (*mcl-1*$^{flox/flox}$*prkdc*$^{scid/scid}$*alb-cre*) by mating hepatocyte-specific Mcl-1-knock-out mice (*bcl-x*$^{flox/flox}$*alb-cre*) and NOD/ShiJic-*scid* Jcl mice. Genotyping of *prkdc*^{scid} gene mutation was performed by the PCR-confronting two-pair primer (PCR-CTPP) method reported previously (19). The mice were maintained in a specific pathogen-free facility and were afforded humane care under approval from the Animal Care and Use Committee of Osaka University Medical School.

Histological Analyses—Liver sections were stained with hematoxylin and eosin (H&E). To detect apoptotic cells, the liver sections were also subjected to staining by terminal deoxynucleotidyltransferase-mediated deoxyuridine triphosphate nick-end labeling (TUNEL) according to a procedure reported previously (20). For immunohistochemical detection of cleaved caspase-3, the liver sections were incubated with the polyclonal rabbit anti-cleaved caspase-3 antibody (Cell Signaling Technology, Beverly, MA) according to a procedure reported previously (20).

Caspase-3/7 Activity—Serum caspase-3/7 activity was measured by a luminescent substrate assay for caspase-3 and caspase-7 (Caspase-Glo assay, Promega) according to the manufacturer's protocol.

Western Blot Analysis—Liver tissue was lysed in lysis buffer (1% Nonidet P-40, 0.5% sodium deoxycholate, 0.1% SDS, 1× protein inhibitor mixture (Nacalai tesque, Kyoto, Japan), 1× phosphatase inhibitor mixture (Nacalai tesque), and phosphate-buffered saline, pH 7.4). The liver lysates were cleared by centrifugation at 10,000 × *g* for 15 min at 4 °C. The protein concentrations were determined using a bicinchoninic acid protein assay kit (Pierce). The protein lysates were electrophoretically separated with SDS-polyacrylamide gels and were transferred onto a polyvinylidene fluoride membrane. For immunodetection, the following antibodies were used: a rabbit polyclonal antibody to Bcl-xL (Santa Cruz Biotechnology, Inc.), a rabbit polyclonal antibody to Bid, a rabbit polyclonal antibody to Bax, a rabbit polyclonal antibody to cleaved caspase-3, a rabbit polyclonal antibody to cleaved caspase-7, a rabbit polyclonal antibody to Puma (Cell Signaling Technology, Beverly, MA), a rabbit monoclonal antibody to Bad, a rabbit polyclonal antibody to Noxa (Abcam, Cambridge, MA), a rabbit polyclonal antibody to Bak (Millipore, Billerica, MA), a rabbit polyclonal antibody to Bim (Enzo Life Sciences Inc., Farmingdale, NY), a rabbit polyclonal antibody to Mcl-1 (Rockland, Gilbertsville, PA), and a mouse monoclonal antibody to β-actin (Sigma-Aldrich).

Real-time Reverse Transcription Polymerase Chain Reaction (Real-time RT-PCR) for mRNA—Total RNA was extracted from liver tissues using an RNeasy minikit (Qiagen, Valencia, CA), was reverse-transcribed, and was subjected to real-time RT-PCR as described previously (21). The mRNA expression of specific genes was quantified using TaqMan gene expression assays (Applied Biosystems, Foster City, CA) as follows: murine *bcl2l11* (assay ID: Mm00437796_m1), murine *fas* (assay ID: Mm01204974_m1), murine *bik* (assay ID: Mm00476123_m1), murine *hrk* (assay ID: Mm01208086_m1), murine *bmf* (assay ID: Mm00506773_m1), and murine *actb* (assay ID: Mm02619580_g1 or Mm00607939_s). The transcript levels are presented as -fold inductions.

siRNA-mediated in Vivo Knockdown—The hepatocyte-specific Bcl-xL-knock-out mice (*bcl-x*$^{flox/flox}$*alb-cre*) and the Bcl-xL/Bim/Bid triple knock-out mice (*bim*$^{-/-}$*bid*$^{-/-}$*bcl-x*$^{flox/flox}$*alb-cre*) were injected with 5 mg/kg *in vivo* grade siRNA against *mcl-1* (MSS275671_e0N), which was mixed with Invivofectamine (Invitrogen), via the tail vein according to the manufacturer's protocol. The mice were sacrificed and examined as indicated by the time courses. The Stealth RNAi negative control with low GC content (Invitrogen) was used as the control.

In Vivo ABT-737 Experiment—ABT-737 was dissolved in a mixture of 30% propylene glycol, 5% Tween 80, and 65% D5W (5% dextrose in water) with pH 4–5. ABT-737 (100 mg/kg) was intraperitoneally administered to the Bim/Bid double knock-

out mice ($bim^{-/-}bid^{-/-}$) or to the Bid-knock-out mice ($bid^{-/-}$). The mice were sacrificed and examined 6 h later.

Statistical Analysis—All of the data are expressed as means ± S.D. unless otherwise indicated. Statistical analyses were performed using an unpaired Student's *t* test or a one-way analysis of variance unless otherwise indicated. When the analyses of variance were applied, the differences in the mean values among the groups were examined by Scheffe's post hoc correction unless otherwise indicated. $p < 0.05$ was considered statistically significant.

RESULTS

The Disruption of Bim Alleviated Spontaneous Hepatocyte Apoptosis in Hepatocyte-specific Bcl-xL-knock-out Mice—To investigate the involvement of the BH3-only protein Bim in the hepatocyte apoptosis caused by Bcl-xL deficiency, hepatocyte-specific Bcl-xL-knock-out mice ($bcl\text{-}x^{fl/fl}alb\text{-}cre$) were mated with systemic Bim-knock-out mice ($bim^{-/-}$). Offspring from the mating of $bim^{+/-}bcl\text{-}x^{fl/fl}alb\text{-}cre$ mice and $bim^{+/-}bcl\text{-}x^{fl/fl}$ mice were examined at 6 weeks of age. A Western blot study confirmed the disappearance of both Bcl-xL and Bim protein expression in the liver tissue of the double knock-out mice ($bim^{-/-}bcl\text{-}x^{fl/fl}alb\text{-}cre$) (Fig. 1*A*). In agreement with our previous report (7, 17), H&E staining of the liver sections showed an increase in the number of hepatocytes, with chromatin condensation and cytosolic shrinkage in the liver lobules of the Bcl-xL-knock-out mice (Fig. 1*B*). The staining also showed a significant increase in TUNEL-positive cells and cleaved caspase-3-positive cells in the liver (Fig. 1, *B–D*). Consistent with these histological observations, the levels of serum caspase-3/7 activity and serum alanine aminotransferase (ALT), which can be used as indicators of hepatocyte apoptosis (22, 23), were significantly higher in the Bcl-xL-knock-out mice than in their wild-type littermates (Fig. 1, *E* and *F*). Additionally, cleaved caspse-3 and -7 were detected in the livers of the Bcl-xL-knock-out mice by Western blotting (Fig. 1*A*). All of these findings indicated spontaneous hepatocyte apoptosis in these mice. Bim-knock-out mice did not show any phenotypes in the liver under physiological conditions (Fig. 1, *B–F*). Alternatively, the disruption of Bim significantly improved all of the parameters that are indicative of hepatocyte apoptosis in Bcl-xL-knock-out mice, including the TUNEL-positive cell counts, cleaved caspase-3-positive cell counts, serum ALT levels, and serum caspase-3/7 activity (Fig. 1, *B–F*). These findings clearly demonstrated that Bim was involved in the hepatocyte apoptosis caused by Bcl-xL disruption. It should be noted that the gene and protein expression levels of Bim were not different between the Bcl-xL-knock-out mice and their wild-type littermates (Fig. 1, *A* and *G*), indicating that the Bim expression levels observed in the healthy liver could induce hepatocyte apoptosis in the absence of the Bcl-2 family proteins.

The Disruption of Bim Alleviated Spontaneous Hepatocyte Apoptosis in Hepatocyte-specific Mcl-1-knock-out Mice—Of the five members of the anti-apoptotic Bcl-2 family proteins, we previously reported that Mcl-1 and Bcl-xL played a pivotal anti-apoptotic role in maintaining hepatocyte integrity in the healthy liver (13). We thus examined the role of Bim in the hepatocyte apoptosis caused by Mcl-1 deficiency. We generated Mcl-1/Bim double knock-out mice ($bim^{-/-}mcl\text{-}1^{fl/fl}alb\text{-}cre$) by mating the hepatocyte-specific Mcl-1-knock-out mice ($mcl\text{-}1^{fl/fl}alb\text{-}cre$) with the systemic Bim-knock-out mice ($bim^{-/-}$). A Western blot study confirmed the disappearance of both Mcl-1 and Bim protein expression in the liver tissue of the double knock-out mice ($bim^{-/-}mcl\text{-}1^{fl/fl}alb\text{-}cre$) (Fig. 2*A*). Consistent with our previous report (13), hepatocyte-specific Mcl-1-knock-out mice showed apoptosis phenotypes very similar to those of the Bcl-xL-knock-out mice, as assessed by TUNEL staining (Fig. 2, *B* and *C*), cleaved caspase-3 staining (Fig. 2, *B* and *D*), serum caspase-3/7 activity (Fig. 2*E*), and serum ALT levels (Fig. 2*F*). In contrast, Mcl-1/Bim double knock-out mice showed significant improvement in these parameters (Fig. 2, *B–F*), indicating that Bim is also involved in the hepatocyte apoptosis induced by the disruption of Mcl-1.

The Disruption of Bim and Bid Prevented Spontaneous Hepatocyte Apoptosis in Hepatocyte-specific Bcl-xL-knock-out Mice—We previously reported that a small amount of Bid, which is another BH3-only protein, was constitutively active and was involved in the spontaneous hepatocyte apoptosis in Bcl-xL- or Mcl-1-knock-out mice (7, 13). We thus examined whether these BH3-only proteins redundantly or cooperatively promoted hepatocyte apoptosis in the absence of Bcl-xL. To this end, Bim/Bid/Bcl-xL triple knock-out mice ($bim^{-/-}bid^{-/-}bcl\text{-}x^{fl/fl}alb\text{-}cre$) were generated by mating the Bim/Bcl-xL double knock-out mice ($bim^{-/-}bcl\text{-}x^{fl/fl}alb\text{-}cre$) with the Bid/Bcl-xL double knock-out mice ($bid^{-/-}bcl\text{-}x^{fl/fl}alb\text{-}cre$). The offspring from the mating of $bim^{+/-}bid-/-bcl\text{-}x^{fl/fl}alb\text{-}cre$ mice with $bim^{+/-}bid^{-/-}bcl\text{-}x^{fl/fl}$ mice were examined at 6 weeks of age. A Western blot study confirmed that Bcl-xL, Bid, and Bim protein expression disappeared from the liver tissue of the triple knock-out mice ($bim^{-/-}bid^{-/-}bcl\text{-}x^{fl/fl}alb\text{-}cre$) (Fig. 3*A*). Liver sections of the Bim/Bid/Bcl-xL triple knock-out mice were histologically normal compared with those of the Bid/Bcl-xL double knock-out mice ($bim^{+/+}bid^{-/-}bcl\text{-}x^{fl/fl}alb\text{-}cre$), which still contained some hepatocytes with apoptotic morphologies (Fig. 3*B*). Both the number of TUNEL-positive cells and the serum caspase-3/7 activity in the triple knock-out mice were significantly lower than those in the Bid/Bcl-xL double knock-out mice and did not differ from their control Bid-knock-out or Bim/Bid double knock-out littermates (Fig. 3, *B–D*). Moreover, in contrast to the mild elevation of serum ALT levels in the Bid/Bcl-xL double knock-out mice, the levels in the triple knock-out mice were completely normal (Fig. 3*E*). These findings demonstrated that hepatocyte apoptosis in the absence of Bcl-xL was completely dependent on these two BH3-only proteins.

Bim and Bid Are Essential Regulators for the Promotion of the Intrinsic Pathway of Apoptosis in Hepatocytes in the Absence of Anti-apoptotic Bcl-2 Family Proteins—We then attempted to further examine the involvement of Bim and Bid in hepatocyte apoptosis in the absence of both Bcl-xL and Mcl-1, which are two major anti-apoptotic proteins in the liver. Because, as we reported (13), the hepatocyte-specific Bcl-xL and Mcl-1 double knock-out mice died within 1 day after birth due to impaired liver development, we performed an siRNA-mediated *in vivo* knockdown of *mcl-1* in the Bcl-xL-knock-out mice and in the Bim/Bid/Bcl-xL triple knock-out mice. *mcl-1* siRNA administration efficiently reduced Mcl-1 protein expression in the liver

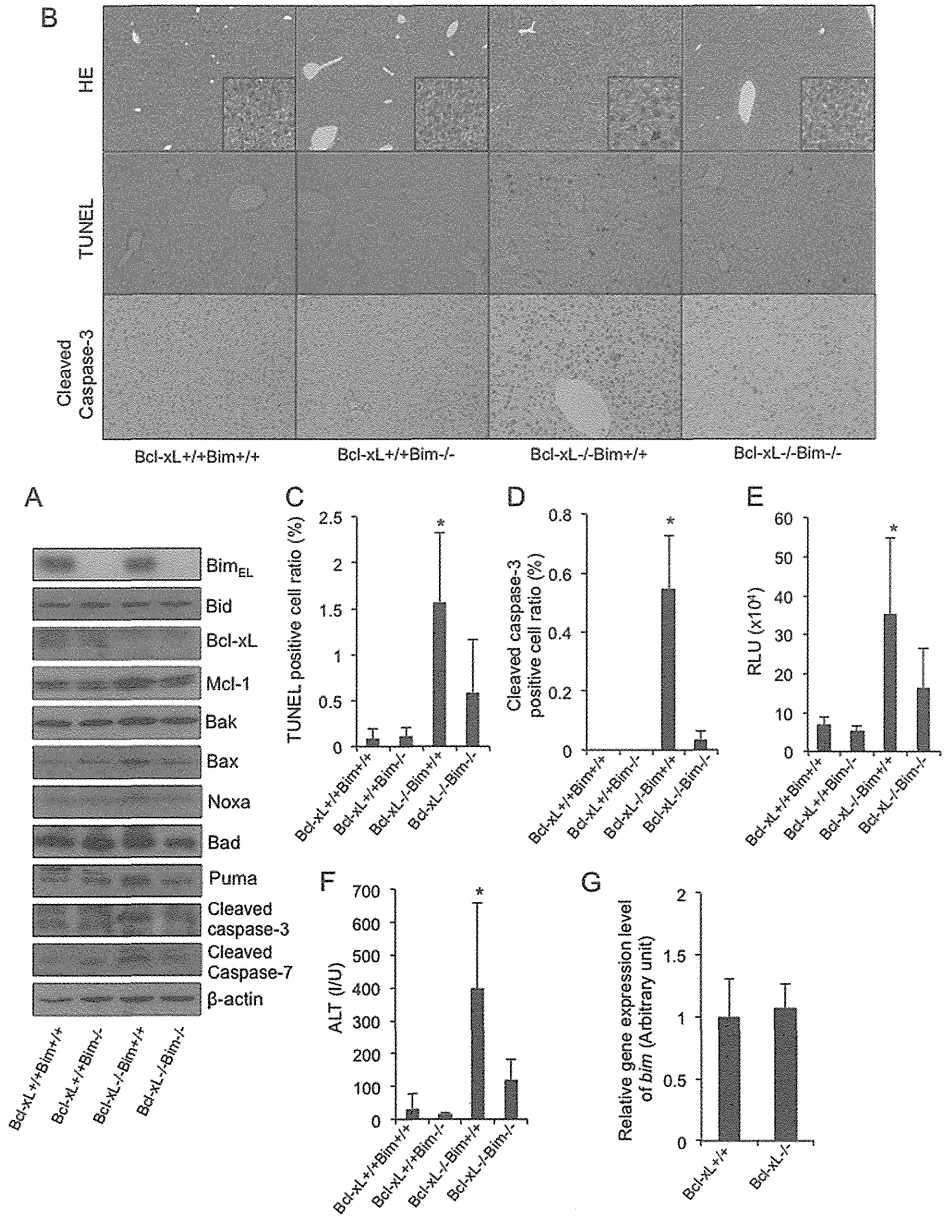

FIGURE 1. **The disruption of Bim alleviated spontaneous hepatocyte apoptosis in the absence of Bcl-xL.** *A–F*, the offspring from the mating of *bim*±*bcl-x*$^{flox/flox}$*alb-cre* mice with *bim*±*bcl-x*$^{flox/flox}$ mice were examined at 6 weeks of age. *Bcl-xL*$^{+/+}$ and *Bcl-xL*$^{-/-}$, *bcl-x*$^{flox/flox}$ and *bcl-x*$^{flox/flox}$*alb-cre*, respectively. *A*, Western blot analysis of whole liver lysates for the expression of Bim$_{EL}$, Bid, Bcl-xL, Mcl-1, Bak, Bax, Noxa, Bad, Puma, cleaved caspase-3, cleaved caspase-7, and β-actin. *B*, representative images for liver histology stained with hematoxylin-eosin (*HE*), TUNEL, and cleaved caspase-3 (original magnifications, ×100 (*large panels*) and ×400 (*insets*)); *black arrows* indicate apoptotic bodies. *C*, TUNEL-positive cell ratio; $n = 8$ mice/group; *, $p < 0.05$ *versus* all. *D*, cleaved caspase-3-positive cell ratio; $n = 3$ mice/group; *, $p < 0.05$ *versus* all. *E*, serum caspase-3/7 activity; $n = 11$ mice/group; *, $p < 0.05$ *versus* all. *F*, serum ALT levels; $n = 13$ mice/group; *, $p < 0.05$ *versus* all. *G*, offspring from the mating of *bcl-x*$^{flox/flox}$*alb-cre* mice with *bcl-x*$^{flox/flox}$ mice were examined at 6 weeks of age. *Bcl-xL*$^{+/+}$ and *Bcl-xL*$^{-/-}$, *bcl-x*$^{flox/flox}$ and *bcl-x*$^{flox/flox}$*alb-cre*, respectively. *bim* mRNA levels in the whole liver tissue were determined by real-time RT-PCR; $n = 6$ mice/group. *Error bars*, S.D. *RLU*, relative light units; *I/U*, international units.

tissue of both mice (Fig. 4*A*), but it caused severe liver injury only in the Bcl-xL-knock-out mice (Fig. 4*B*) when assessed by the H&E staining of liver sections. Notably, *mcl-1* siRNA administration caused massive hepatocyte apoptosis in the Bcl-xL-knock-out mice, but this apoptosis was weakened in the Bim/Bid/Bcl-xL triple knock-out mice, as evidenced by the TUNEL staining of the liver sections, serum caspase-3/7 activity, and serum ALT levels (Fig. 4, *C–E*). In agreement with these findings, *mcl-1* siRNA treatment impaired the liver function of the Bcl-xL-knock-out mice, as evidenced by an increase in the serum bilirubin levels, but not the liver function of the triple knock-out mice (Fig. 4*F*). These findings demonstrated that the massive hepatocyte apoptosis and liver failure caused by decreases in these anti-apoptotic Bcl-2 family proteins were dependent on Bid and Bim.

The Presence of Bim- and Bid-induced Constant BH3 Stress in the Healthy Liver Causes Hepatotoxicity with the Use of Anti-cancer Agents That Target the Anti-apoptotic Bcl-2 Family Proteins—Recent advances in cancer therapy have enabled the selective targeting of some anti-apoptotic Bcl-2 family proteins,

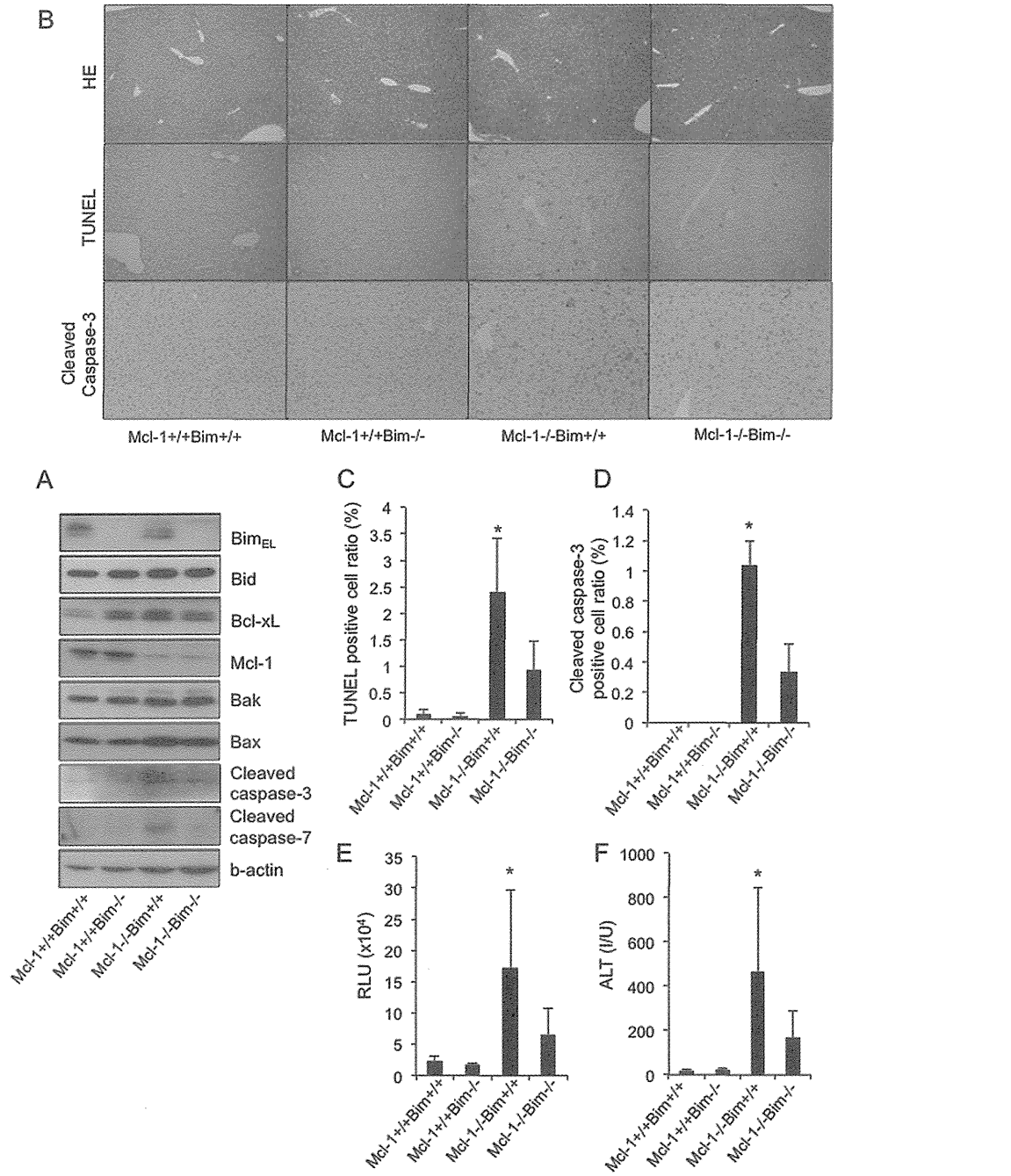

FIGURE 2. **The disruption of Bim alleviated spontaneous hepatocyte apoptosis in the absence of Mcl-1.** The offspring from the mating of *bim*$^{+-}$*mcl-1*$^{flox/flox}$*alb-cre* mice with *bim*$^{+/-}$*mcl-1*$^{flox/flox}$ mice were examined at 6 weeks of age. *Mcl-1*$^{+/+}$ and *Mcl-1*$^{-/-}$, *mcl-1*$^{flox/flox}$ and *mcl-1*$^{flox/flox}$*alb-cre*, respectively. *A*, Western blot analysis of whole liver lysates for the expression of Bim$_{EL}$, Bid, Bcl-xL, Mcl-1, Bak, Bax, cleaved caspase-3, cleaved caspse-7, and β-actin. *B*, representative images for liver histology stained with hematoxylin-eosin (*HE*), TUNEL, and cleaved caspase-3 (original magnification, ×100). *C*, TUNEL-positive cell ratio; $n = 3$–6 mice/group; *, $p < 0.05$ *versus* all. *D*, cleaved caspase-3-positive cell ratio; $n = 3$ mice/group; *, $p < 0.05$ *versus* all. *E*, serum caspase-3/7 activity; $n = 9$–15 mice/group; *, $p < 0.05$ *versus* all. *F*, serum ALT levels; $n = 9$–15 mice/group; *, $p < 0.05$ *versus* all. *Error bars*, S.D. *RLU*, relative light units; *I/U*, international units.

which are often dysregulated in malignant cells. ABT-737, which is a BH3 mimetic, could inhibit Bcl-xL, Bcl-2, and Bcl-w, and it has induced the regression of solid tumors (23). We previously reported that high dose ABT-737 administration caused hepatocyte apoptosis even in a normal liver, which was partly due to constitutive Bid-mediated BH3 stress (7). This finding led us to investigate the involvement of Bim and Bid in this ABT-737-mediated hepatotoxicity. Bim/Bid double knock-out mice (*bim*$^{-/-}$*bid*$^{-/-}$) were generated by mating Bim knock-out mice (*bim*$^{-/-}$) with Bid knock-out mice (*bid*$^{-/-}$), and the offspring were then treated with this drug. Western blot analysis confirmed the efficient deletion of Bim and Bid from the liver tissue of the double knock-out mice (Fig. 5*A*). Upon ABT-737 treatment, the Bim/Bid double knock-out mice showed complete prevention of ABT-737-induced hepatocyte apoptosis and hepatotoxicity (Fig. 5, *B–F*), in sharp con-